

**Features:**

chicken B-actin promoter/enhancer: bases 18–1,718
 pCAGGF2 primer: bases 1,666–1,685
 mCherry gene: bases 1,778–2,488
 rabbit beta-globin polyT: bases 2,589–3,056
 polyT(167)rev primer: bases 2,740–2,759
 ampicillin resistance gene: bases 4,608–5,468

reference:**sequencing primers:**

CAGGS-F2: TACAGCTCCTGGGCAACGTG
 polyAT(167)rev: CCC ATA TGT CCT TCC GAG TG
 RFP (upper nested): GAGTTCATGCGCTTCAAGGT
 RFP (lower nested): CCCATGGTCTTCTTCTGCAT

suitable bacteria: TOP10 or DH5alpha

antibiotic: ampicillin/carbenecillin

Notes:

The mCherry open reading frame was created by PCR amplification of the mCherry-N1 plasmid. Since this plasmid has no start site an initiator ATG was added to the forward primer. After PCR amplification mCherry was inserted into the directional pENTR-D-TOPO gateway cloning vector. (+) Colonies were selected by PCR and confirmed by sequencing. 100ng of purified plasmid was mixed with pCAGG-DV destination vector in the presence of LR clonase II. After recombination clones were selected and sequenced.

mcherry start(noATG): GTGAGCAAGGGCGAGGAGGATA

mcherry start(w/ATG): CACCATGGTGAGCAAGGGCGAGGAGGATA

mcherry Rev: TTTACTTATACAGCTCGTCCA

LOCUS	mCherryCAGG	5599 bp	XXX	UPDATED	16-Jul-2008	00:31
DEFINITION	mCherryCAGG plasmid	sequence (1-5599)				
ORIGIN						
1	GTCGACATTG	ATTATTGACT	AGTTATTAAT	AGTAATCAAT	TACGGGGTCA	TTAGTTCATA
61	GCCCATATAT	GGAGTTCGCG	GTTACATAAC	TTACGGTAAA	TGGCCCGCCT	GGCTGACCGC
121	CCAACGACCC	CCGCCATTG	ACGTCAATAA	TGACGTATGT	TCCCATAGTA	ACGCCAATAG
181	GGACTIONTCCA	TTGACGTCAA	TGGGTGGACT	ATTTACGGTA	AACTGCCAC	TTGGCAGTAC
241	ATCAAGTGTA	TCATATGCCA	AGTACGCCCC	CTATTGACGT	CAATGACGGT	AAATGGCCCG
301	CCTGGCATT	TGCCAGTAC	ATGACCTTAT	GGGACTTTCC	TACTTGGCAG	TACATCTACG
361	TATTAGTCAT	CGCTATTACC	ATGGGTTCGAG	GTGAGCCCCA	CGTTCGCTT	CACTCTCCCC
421	ATCTCCCCC	CCTCCCCACC	CCCAATTTTG	TATTTATTTA	TTTTTTAATT	ATTTTGTGCA
481	GCGATGGGGG	CGGGGGGGGG	GGGGGCGCGC	GCCAGGCGGG	GCGGGGCGGG	GCGAGGGGGC
541	GGGCGGGGGC	AGGCGGAGAG	GTGCGGCGGC	AGCCAATCAG	AGCGGCGCGC	TCCGAAAGTT
601	TCCTTTTATG	GCGAGGCGGC	GGCGGCGGCG	GCCCTATAAA	AAGCGAAGCG	CGCGGCGGGC
661	GGGAGTCGCT	GCGTTGCCTT	CGCCCCGTGC	CCCCTCCGC	GCCGCTCGC	GCCGCCCGCC
721	CCGGCTCTGA	CTGACCGCGT	TACTCCACA	GGTGAGCGGG	CGGGACGGCC	CTTCTCCTCC
781	GGGCTGTAAT	TAGCGCTTGG	TTAATGACG	GCTCGTTTCT	TTTCTGTGGC	TGCGTGAAAG
841	CCTTAAAGGG	CTCCGGGAGG	GCCCTTTGTG	CGGGGGGGAG	CGGCTCGGGG	GGTGCGTGCG
901	TGTGTGTGTG	CGTGGGGAGC	GCCGCGTGC	GCCCGCGCTG	CCCGGCGGCT	GTGAGCGCTG
961	CGGGCGCGGC	GCGGGGCTTT	GTGCGCTCCG	CGTGTGCGCG	AGGGGAGCGC	GGCCGGGGGC
1021	GGTGCCCGC	GGTGCGGGGG	GGCTGCGAGG	GGAACAAAGG	CTGCGTGCGG	GGTGTGTGCG
1081	TGGGGGGGTG	AGCAGGGGGT	GTGGGCGCGG	CGGTGCGGGT	GTAACCCCC	CCTGCACCCC
1141	CCTCCCGAG	TTGCTGAGCA	CGGCCCGGCT	TCGGGTGCGG	GGCTCCGTGC	GGGGCGTGCC
1201	GCGGGGCTCG	CCGTGCCGGG	CGGGGGGTGG	CGGCAGGTGG	GGGTGCCGGG	CGGGGCGGGG
1261	CCGCTCGGG	CCGGGGAGGG	CTCGGGGGAG	GGGCGCGGCG	GCCCGGAGC	GCCGCGGGCT
1321	GTCGAGGCGC	GGCGAGCCGC	AGCCATTGCC	TTTTATGGTA	ATCGTGCGAG	AGGGCGCAGG
1381	GACTIONCCTTT	GTCCCAAATC	TGGCGGAGCC	GAAATCTGGG	AGGCGCCGCC	GCACCCCTC
1441	TAGCGGGCGC	GGGCGAAGCG	GTGCGGCGCC	GGCAGGAAGG	AAATGGGCGG	GGAGGGCCTT
1501	CGTGCGTCGC	CGCGCCGCCG	TCCCCTTCTC	CATCTCCAGC	CTCGGGGCTG	CCGCAGGGGG
1561	ACGGCTGCCT	TCGGGGGGGA	CGGGGCAGGG	CGGGGTTCGG	CTTCTGGCGT	GTGACCGGGC
1621	GCTCTAGAGC	CTCTGCTAAC	CATGTTTCATG	CCTTCTTCTT	TTTCTTACAG	CTCCTGGGCA
1681	ACGTGCTGGT	TATTGTGCTG	TCTCATCATT	TTGGCAAAGA	ATTCCCTCGAA	TCACAAGTTT
1741	GTACAAAAA	GCAGGCTCCG	CGGCCGCCCC	CTTACCATG	GTGAGCAAGG	GCGAGGAGGA
1801	TAACATGGCC	ATCATCAAGG	AGTTTCATGCG	CTTCAAGGTG	CACATGGAGG	GCTCCGTGAA
1861	CGGCCACGAG	TTGAGATCG	AGGGCGAGGG	CGAGGGCCGC	CCCTACGAGG	GCACCCAGAC
1921	CGCCAAGCTG	AAGGTGACCA	AGGGTGGCCC	CCTGCCCTTC	GCCTGGGACA	TCCTGTCCCC
1981	TCAGTTTCATG	TACGGCTCCA	AGGCCTACGT	GAAGCACCCC	GCCGACATCC	CCGACTACTT
2041	GAAGCTGTCC	TTCCCCGAGG	GCTTCAAGTG	GGAGCGCGTG	ATGAACTTCG	AGGACGGCGG
2101	CGTGGTGACC	GTGACCCAGG	ACTCCTCCCT	GCAGGACGGC	GAGTTCATCT	ACAAGGTGAA
2161	GCTGCGCGGC	ACCAACTTCC	CCTCCGACGG	CCCCGTAATG	CAGAAGAAGA	CCATGGGCTG
2221	GGAGGCCTCC	TCCGAGCGGA	TGTACCCCGA	GGACGCGGCC	CTGAAGGGCG	AGATCAAGCA
2281	GAGGCTGAAG	CTGAAGGACG	GCGGCCACTA	CGACGCTGAG	GTCAAGACCA	CCTACAAGGC
2341	CAAGAAGCCC	GTGCAGCTGC	CCGGCGCCTA	CAACGTCAAC	ATCAAGTTGG	ACATCACCTC
2401	CCACAACGAG	GACTACACCA	TCGTGGAACA	GTACGAACGC	GCCGAGGGCC	GCCACTCCAC
2461	CGGCGGCATG	GACGAGCTGT	ATAAGTAAAA	GGGTGGGCGC	GCCGACCCAG	CTTTCTTGTA
2521	CAAAGTGGTG	ATTCGAGGAA	TTCACTCCTC	AGGTGCAGGC	TGCCATATCAG	AAGGTGGTGG
2581	CTGGTGTGGC	CAATGCCCTG	GCTCACAAAT	ACCACTGAGA	TCTTTTTTCCC	TCTGCCAAAA
2641	ATTATGGGGA	CATCATGAAG	CCCCTTGAGC	ATCTGACTTC	TGGCTAATAA	AGGAAATTTA
2701	TTTTCAATTGC	AATAGTGTGT	TGGAATTTTT	TGTGTCTCTC	ACTCGGAAGG	ACATATGGGA
2761	GGGCAAATCA	TTTAAACAT	CAGAATGAGT	ATTTGGTTTA	GAGTTTGGA	ACATATGCC
2821	ATATGCTGGC	TGCCATGAAC	AAAGGTTGGC	TATAAAGAGG	TCATCAGTAT	ATGAAACAGC
2881	CCCCTGCTGT	CCATTCTT	TTCCATAGAA	AAGCCTTGAC	TTGAGGTTAG	ATTTTTTTTA
2941	TATTTTGT	TGTGTTATTT	TTTTCTTTAA	CATCCCTAAA	ATTTTCTT	CATGTTTTAC
3001	TAGCCAGATT	TTTCTCTC	TCCTGACTAC	TCCAGTCAT	AGCTGTCCCT	CTTCTCTTAT
3061	GGAGATCCCT	CGACCTGCAG	CCCAAGCTTG	GCGTAATCAT	GGTCATAGCT	GTTTCTGTG
3121	TGAAATTGTT	ATCCGCTCAC	AATTCCACAC	AACATACGAG	CCGGAAGCAT	AAAGTGTA
3181	GCCTGGGGTG	CCTAATGAGT	GAGCTAACTC	ACATTAATTG	CGTTGCGCTC	ACTGCCCGCT
3241	TTCCAGTCGG	GAAACCTGTC	GTGCCAGCGG	ATCCGCATCT	CAATTAGTCA	GCAACCATAG
3301	TCCCGCCCCT	AACTCCGCC	ATCCCGCCCC	TAACTCCGCC	CAGTTCGCC	CATTCTCCGC
3361	CCCATGGCTG	ACTAATTTTT	TTTATTTATG	CAGAGGCCGA	GGCCGCTCG	GCCTCTGAGC
3421	TATTCCAGAA	GTAGTGAGGA	GGTTTTTTTG	GAGGCCTAGG	CTTTTGCAA	AAGCTAACTT

3481 GTTTATTGCA GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAAATT TCACAAATAA
3541 AGCATTTTTT TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATG TATCTTATCA
3601 TGTCTGGATC CGCTGCATTA ATGAATCGGC CAACGCGCGG GGAGAGGCGG TTTGCGTATT
3661 GGGCGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT CGGTCGTTCG GCTGCGGCGA
3721 GCGGTATCAG CTCACTCAAA GGCGGTAATA CGGTTATCCA CAGAATCAGG GGATAACGCA
3781 GGAAAGAACA TGTGAGCAAA AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG
3841 CTGGCGTTTT TCCATAGGCT CCGCCCCCT GACGAGCATC AAAAAAATCG ACGCTCAAGT
3901 CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATAACCAGG CGTTTCCCCC TGGAAGCTCC
3961 CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT ACCTGTCCGC CTTTCTCCCT
4021 TCGGGAAGCG TGGCGCTTTC TCAATGCTCA CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC
4081 GTTCGCTCCA AGCTGGGCTG TGTGCACGAA CCCCCCGTTC AGCCCGACCG CTGCGCCTTA
4141 TCCGTAACCT ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA
4201 GCCACTGGTA ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG
4261 TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC TCTGCTGAAG
4321 CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG GCAAACAAAC CACCGCTGGT
4381 AGCGGTGGTT TTTTTGTTT CAAGCAGCAG ATTACGCGCA GAAAAAAGG ATCTCAAGAA
4441 GATCCTTTGA TCTTTTCTAC GGGGTCTGAC GCTCAGTGGG ACGAAAACCTC ACGTTAAGGG
4501 ATTTTGGTCA TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA
4561 AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA CCAATGCTTA
4621 ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTTCGTT CATCCATAGT TGCCTGACTC
4681 CCCGTCGTGT AGATAACTAC GATACGGGAG GGCTTACCAT CTGGCCCCAG TGCTGCAATG
4741 ATACCGCGAG ACCCACGCTC ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA
4801 AGGGCCGAGC GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT
4861 TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT TGTTGCCATT
4921 GCTACAGGCA TCGTGGTGTG ACGCTCGTCG TTTGGTATGG CTTCATTCAG CTCCGGTTCC
4981 CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC
5041 GGTCTCCGA TCGTTGTCAG AAGTAAGTTG GCCGCAGTGT TACTACTCAT GGTATGGCA
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5161 TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC TTGCCCGGCG
5221 TCAATACGGG ATAATACCGC GCCACATAGC AGAACTTTAA AAGTGCTCAT CATTTGAAAA
5281 CGTTCTTCGG GGCGAAAACT CTCAAGGATC TTACCGCTGT TGAGATCCAG TTCGATGTAA
5341 CCCACTCGTG CACCCAACCTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA
5401 GCAAAAACAG GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA
5461 ATACTCATAC TCTTCCTTTT TCAATATTTAT TGAAGCATTT ATCAGGGTTA TTGTCTCATG
5521 AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA TAGGGGTTCC GCGCACATTT
5581 CCCCAAAAAG TGCCACCTG

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features_seq

>chicken B-actin promoter/enhancer

ACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGGTTACATAACTTACGG
TAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCC
AATAGGGACTTTCATTGACGTCAATGGGTGGACTATTTACGTTAACTGCCACTTGGCAGTACATCAAGTGTATCAT
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CGGCTTCTGGCGTGTGACCGGCGGCTCTAGAGCCTCTGCTAACCATGTTTCATGCCTTCTTCTTTTCTTACAGCTCCTG
GGCAACGTGCTGTTTATTGTGCTGTCTCATCATTTTGCAA

>pCAGGF2 sequencing primer

TACAGCTCCTGGCAACGTG

>mCherry open reading frame

ATGGTGAGCAAGGGCGAGGAGGATAACATGGCCATCATCAAGGAGTTCATGCGCTTCAAGGTGCACATGGAGGGCTCCG
TGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCTACGAGGGCACCCAGACCGCCAAGCTGAAGGT
GACCAAGGGTGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCTCAGTTCATGTACGGCTCCAAGGCCTACGTGAAG
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ACGGCGGCGTGGTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCGAGTTCATCTACAAGGTGAAGCTGCGCGGCAC
CACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCTCCGAGCGGATGTACCCCGAG
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CCTACAAGGCCAAGAAGCCCGTGCAGCTGCCCGGCGCCTACAACGTCAACATCAAGTTGGACATCACCTCCACAACGA
GGACTACACCATCGTGGAACAGTACGAACGCGCCGAGGGCCGCACTCCACCGGCGGCATGGACGAGCTGTATAAGTAA

>rabbit B-globin polyT

GCCAATGCCCTGGCTCACAAATACCACTGAGATCTTTTTCCCTCTGCCAAAAATTATGGGGACATCATGAAGCCCTTG
AGCATCTGACTTCTGGCTAATAAAGGAAATTTATTTTCATTGCAATAGTGTGTTGGAATTTTTTGTGTCTCTCACTCGG
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TTCTTACATGTTTTACTAGCCAGATTTTTTCTCCTCTCCTGACTACTCCAGTCATAGCTGTCCCTCTTCTC

>ampicillin resistance gene

TTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTC
GTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGG
CTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTTCAACTTTATCCGCTCCAT
CCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTAAATAGTTTGCGCAACGTTGTTGCCATTGCT
ACAGGCATCGTGGTGTACGCTCGTCTTTGGTATGGCTTCATTCAGCTCCGTTCCCAACGATCAAGGCGAGTTACAT
GATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCTCCTCGATCGTTGTCAGAAGTAAGTTGGCCGAGTGT
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TGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCAT

Non-cutters

Absent Sites on mCherry-pCAGG

Enzyme	Site	Enzyme	Site	Enzyme	Site
Acc65I	G/GTACC	BstZ17I	GTA/TAC	PflFI	GACN/NGTC
AccIII	T/CCGGA	Bsu15I	AT/CGAT	PinAI	A/CCGGT
AcvI	CAC/GTG	BsuTUI	AT/CGAT	PmaCI	CAC/GTG
AdeI	CACNNN/GTG	BtrI	CAC/GTC	PmeI	GTTT/AAAC
AflIII	C/TTAAG	Cfr9I	C/CCGGG	PmlI	CAC/GTG
AgeI	A/CCGGT	CjuI	CAYNNNNNRTG	Ppu10I	A/TGCAT
AlfI	GCANNNNNNTGC	CjuII	CAYNNNNNCTC	PpuMI	RG/GWCCY
Aor13HI	T/CCGGA	Clal	AT/CGAT	PshAI	GACNN/NGTC
AsiGI	A/CCGGT	CpoI	CG/GWCCG	Psp124BI	GAGCT/C
AsiSI	GCGAT/CGC	Csp45I	TT/CGAA	Psp5II	RG/GWCCY
Asp718I	G/GTACC	CspAI	A/CCGGT	PspCI	CAC/GTG
AspI	GACN/NGTC	CspCI	CAANNNNNGTGG	PspLI	C/GTACC
AsuII	TT/CGAA	CspI	CG/GWCCG	PspPPI	RG/GWCCY
AsuNHI	G/CTAGC	DraIII	CACNNN/GTG	PspXI	VC/TCGAGB
AvaIII	ATGCAT	DrdII	GAACCA	PsrI	GAACNNNNNTAC
BaeI	ACNNNNGTAYC	Ecl136II	GAG/CTC	PsyI	GACN/NGTC
BanIII	AT/CGAT	Eco32I	GAT/ATC	RgaI	GCGAT/CGC
BbrPI	CAC/GTG	Eco72I	CAC/GTG	Rsr2I	CG/GWCCG
BbuI	GCATG/C	EcoICRI	GAG/CTC	RsrII	CG/GWCCG
BclI	T/GATCA	EcoNI	CCTNN/NNNAGG	SacI	GAGCT/C
BfrI	C/TTAAG	EcoRV	GAT/ATC	SanDI	GG/GWCCC
BlfI	T/CCGGA	EcoT22I	ATGCA/T	SciI	CTC/GAG
BmgBI	CAC/GTC	Esp3I	CGTCTC	SexAI	A/CCWGGT
BmtI	GCTAG/C	FbaI	T/GATCA	Sfr274I	C/TCGAG
BoxI	GACNN/NGTC	FseI	GGCCGG/CC	SfuI	TT/CGAA
Bpul4I	TT/CGAA	FspAI	RTGC/GCAY	SgfI	GCGAT/CGC
Bsa29I	AT/CGAT	HpaI	GTT/AAC	SgrDI	CGTCGACG
BseAI	T/CCGGA	Kpn2I	T/CCGGA	SlaI	C/TCGAG
BseCI	AT/CGAT	KpnI	GGTAC/C	SmaI	CCC/GGG
BshTI	A/CCGGT	Ksp22I	T/GATCA	SmiI	ATTT/AAAT
BsiWI	C/GTACG	KspAI	GTT/AAC	SnaI	GTATAC
BsmBI	CGTCTC	MabI	A/CCWGGT	SphI	GCATG/C
Bsp119I	TT/CGAA	MfeI	C/AATTG	SplI	C/GTACG
Bsp13I	T/CCGGA	MluI	A/CCGGT	SrfI	GCCC/GGGC
Bsp68I	TCG/CGA	Mph1103I	ATGCA/T	Sse8647I	AG/GWCCT
BspDI	AT/CGAT	MroI	T/CCGGA	SstI	GAGCT/C
BspEI	T/CCGGA	MspCI	C/TTAAG	StrI	C/TCGAG
BspGI	CTGGAC	MssI	GTTT/AAAC	SwaI	ATTT/AAAT
BspMII	T/CCGGA	MunI	C/AATTG	TliI	C/TCGAG
BspT104I	TT/CGAA	NheI	G/CTAGC	TstI	CACNNNNNTCC
BspTI	C/TTAAG	NruI	TCG/CGA	Tth111I	GACN/NGTC
BspXI	AT/CGAT	NsiI	ATGCA/T	Vha464I	C/TTAAG
BssNAI	GTA/TAC	NspV	TT/CGAA	XagI	CCTNN/NNNAGG
Bst1107I	GTA/TAC	PacI	TTAAT/TAA	XhoI	C/TCGAG
Bst98I	C/TTAAG	PaeI	GCATG/C	XmaCI	C/CCGGG
BstBI	TT/CGAA	PaeR7I	C/TCGAG	XmaI	C/CCGGG
BstENI	CCTNN/NNNAGG	PasI	CC/CWGGG	Zsp2I	ATGCA/T
BstPAI	GACNN/NGTC	Pfl23II	C/GTACC		

unique restriction sites

mCherry-CAGG

Unique cutters for mCherry-CAGG

Enzyme	Site	5'	Cut	3'
SalI	G/TCGAC	1 (0)	1 (5599)	5599
AccI	GT/MKAC	1 (1)	2 (5598)	5599
FblI	GT/MKAC	1 (1)	2 (5598)	5599
XmiI	GT/MKAC	1 (1)	2 (5598)	5599
AhlI	A/CTAGT	1 (17)	18 (5582)	5599
BcuI	A/CTAGT	1 (17)	18 (5582)	5599
SpeI	A/CTAGT	1 (17)	18 (5582)	5599
BstSNI	TAC/GTA	1 (358)	359 (5241)	5599
Eco105I	TAC/GTA	1 (358)	359 (5241)	5599
SnaBI	TAC/GTA	1 (358)	359 (5241)	5599
PfoI	T/CCNGGA	1 (851)	852 (4748)	5599
Bsp120I	G/GGCC	1 (858)	859 (4741)	5599
PspOMI	G/GGCC	1 (858)	859 (4741)	5599
ApaI	GGCC/C	1 (862)	863 (4737)	5599
BlpI	GC/TNAGC	1 (1153)	1154 (4446)	5599
Bpu1102I	GC/TNAGC	1 (1153)	1154 (4446)	5599
Bsp1720I	GC/TNAGC	1 (1153)	1154 (4446)	5599
CelII	GC/TNAGC	1 (1153)	1154 (4446)	5599
EspI	GC/TNAGC	1 (1153)	1154 (4446)	5599
AarI	CACCTGC	1 (1242)	1243 (4357)	5599
Sse232I	CG/CCGGCG	1 (1310)	1311 (4289)	5599
XbaI	T/CTAGA	1 (1622)	1623 (3977)	5599
CciNI	GC/GGCCGC	1 (1760)	1761 (3839)	5599
NotI	GC/GGCCGC	1 (1760)	1761 (3839)	5599
FalI	AAGNNNNNCTT	1 (2031)	2032 (3568)	5599
AloI	GAACNNNNNTCC	1 (2124)	2125 (3475)	5599
SbfI	CCTGCA/GG	1 (2132)	2133 (3467)	5599
SdaI	CCTGCA/GG	1 (2132)	2133 (3467)	5599
Sse8387I	CCTGCA/GG	1 (2132)	2133 (3467)	5599
BbsI	GAAGAC	1 (2212)	2213 (3387)	5599
BbvII	GAAGAC	1 (2212)	2213 (3387)	5599
BpiI	GAAGAC	1 (2212)	2213 (3387)	5599
BpuAI	GAAGAC	1 (2212)	2213 (3387)	5599
BstV2I	GAAGAC	1 (2212)	2213 (3387)	5599
Bbr7I	GAAGAC	1 (2217)	2218 (3382)	5599
BbvCI	CC/TCAGC	1 (2315)	2316 (3284)	5599
Bpu10I	CC/TNAGC	1 (2315)	2316 (3284)	5599
PvuII	CAG/CTG	1 (2355)	2356 (3244)	5599
XcmI	CCANNNNN/NNNTGG	1 (2463)	2464 (3136)	5599
AscI	GG/CGCGCC	1 (2496)	2497 (3103)	5599
PalAI	GG/CGCGCC	1 (2496)	2497 (3103)	5599
SgsI	GG/CGCGCC	1 (2496)	2497 (3103)	5599
AxyI	CC/TNAGG	1 (2547)	2548 (3052)	5599
Bse21I	CC/TNAGG	1 (2547)	2548 (3052)	5599
Bsu36I	CC/TNAGG	1 (2547)	2548 (3052)	5599
Eco81I	CC/TNAGG	1 (2547)	2548 (3052)	5599
SauI	CC/TNAGG	1 (2547)	2548 (3052)	5599
BstXI	CCANNNNN/NTGG	1 (2596)	2597 (3003)	5599
BglII	A/GATCT	1 (2617)	2618 (2982)	5599
BsbI	CAACAC	1 (2715)	2716 (2884)	5599
AjuI	GAANNNNNNNTTGG	1 (2781)	2782 (2818)	5599
HindIII	A/AGCTT	1 (3083)	3084 (2516)	5599
BsaBI	GATNN/NNATC	1 (3273)	3274 (2326)	5599
Bse8I	GATNN/NNATC	1 (3273)	3274 (2326)	5599
BseJI	GATNN/NNATC	1 (3273)	3274 (2326)	5599
MamI	GATNN/NNATC	1 (3273)	3274 (2326)	5599
SfiI	GGCCNNNN/NGGCC	1 (3407)	3408 (2192)	5599

AspA2I	C/CTAGG	1	(3454)	3455	(2145)	5599
AvrII	C/CTAGG	1	(3454)	3455	(2145)	5599
BlnI	C/CTAGG	1	(3454)	3455	(2145)	5599
XmaJI	C/CTAGG	1	(3454)	3455	(2145)	5599
PsiI	TTA/TAA	1	(3494)	3495	(2105)	5599
BsaMI	GAATGC	1	(3561)	3562	(2038)	5599
BsmI	GAATGC	1	(3561)	3562	(2038)	5599
MvaI269I	GAATGC	1	(3561)	3562	(2038)	5599
PctI	GAATGC	1	(3561)	3562	(2038)	5599
LguI	GCTCTTC	1	(3671)	3672	(1928)	5599
SapI	GCTCTTC	1	(3671)	3672	(1928)	5599
HgiEII	ACCNNNNNNGGT	1	(4367)	4368	(1232)	5599
BsaI	GGTCTC	1	(4753)	4754	(846)	5599
Bso31I	GGTCTC	1	(4753)	4754	(846)	5599
BspTNI	GGTCTC	1	(4753)	4754	(846)	5599
Eco31I	GGTCTC	1	(4753)	4754	(846)	5599
Acc16I	TGC/GCA	1	(4902)	4903	(697)	5599
AviII	TGC/GCA	1	(4902)	4903	(697)	5599
FspI	TGC/GCA	1	(4902)	4903	(697)	5599
MstI	TGC/GCA	1	(4902)	4903	(697)	5599
NsbI	TGC/GCA	1	(4902)	4903	(697)	5599
MvrI	CGAT/CG	1	(5050)	5051	(549)	5599
Ple19I	CGAT/CG	1	(5050)	5051	(549)	5599
PvuI	CGAT/CG	1	(5050)	5051	(549)	5599
AssI	AGT/ACT	1	(5160)	5161	(439)	5599
ScaI	AGT/ACT	1	(5160)	5161	(439)	5599
ZrmI	AGT/ACT	1	(5160)	5161	(439)	5599
BcgI	CGANNNNNNTGC	1	(5184)	5185	(415)	5599
Asp700I	GAANN/NNTTC	1	(5279)	5280	(320)	5599
MroXI	GAANN/NNTTC	1	(5279)	5280	(320)	5599
PdmI	GAANN/NNTTC	1	(5279)	5280	(320)	5599
XmnI	GAANN/NNTTC	1	(5279)	5280	(320)	5599
SspI	AAT/ATT	1	(5484)	5485	(115)	5599